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Sequence identity	Group	Clone nº.	Size Kb	Published Sequence gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ -ID-NO-17	Pulp Upregulated	U-U115	1.5	Pectate Lyase	67.3	508	<i>Zea mays</i> , L20140
SEQ -ID-NO-18	Pulp Upregulated	U-U117	1.7	Pectate Lyase	55.0	333	<i>Lilium longiflorum</i> , Z17328
SEQ -ID-NO-19	Pulp Upregulated	U-U80	0.6	Vicilin-like storage protein	53.7	387	<i>Arabidopsis thaliana</i> , T13642
SEQ -ID-NO-20	Pulp Upregulated	U-U90	1.8	Glutamate Descarboxylase	72.5	735	<i>Petunia hybrida</i> , L16797
SEQ -ID-NO-21	Pulp Upregulated	U-U92	1.8	Glutamate Descarboxylase	71.8	740	<i>Arabidopsis thaliana</i> , U10034
SEQ -ID-NO-22	Pulp Upregulated	U-U91	1.1	Aconitase	76.4	766	Pumpkin (<i>Cucurbita sp.</i>), D29629
SEQ -ID-NO-23	Pulp Upregulated	U-U96	0.9	Express Sequence Tag.	69.0	452	<i>Arabidopsis thaliana</i> , H36910
SEQ -ID-NO-24	Pulp Upregulated	U-U103	2	Cell Wall Invertase	66.0	567	<i>Zea mays</i> , U17695
SEQ -ID-NO-25	Pulp Upregulated	U-U93	3.5	Heat Shock Protein cognate	76.4	711	<i>Lycopersicon esculentum</i> , X54030
SEQ -ID-NO-26	Pulp Upregulated	U-U125	1.8	Heat Shock Protein	71.0	662	<i>Spinacia oleracea</i> , L26243
SEQ -ID-NO-27	Pulp Upregulated	U-U105	0.9	Hexaubiquitin Protein	64.1	237	Sunflower (<i>Helianthus</i> <i>annuus</i>), X57004

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SEQ -ID-NO-28	Pulp Upregulated	U-U116	0.8	Polyubiquitin	81.0	625	Rice (<i>Oryza sativa</i>), X76064
SEQ -ID-NO-29	Pulp Upregulated	U-U120	0.9	Extensin	56.9	576	Almond (<i>Prunus amygdalus</i>), X65718
SEQ -ID-NO-30	Pulp Upregulated	U-U126	1.2	Basic Chitinase	63.2	506	Cowpea (<i>Vigna unguiculata</i>), X88801
SEQ -ID-NO-31	Pulp Upregulated	U-U129	1.3	Beta glucosidase	60.9	517	White clover (<i>Trifolium repens</i>), X56733
SEQ -ID-NO-32	Pulp Upregulated	U-U130	1.3	Chlorophyll a/b binding protein	52.0	415	Rice (<i>Oryza sativa</i>), D00641
SEQ -ID-NO-33	Pulp Upregulated	U-U43	2.5	Fruit sp pp involved in maturation	53.8	396	Tomato (<i>Lycopersicon esculentum</i>), X13743
SEQ -ID-NO-34	Pulp Upregulated	U-U70	0.6	Root specific protein	63.6	420	Rice (<i>Oryza sativa</i>), L227208
SEQ -ID-NO-35	Pulp Upregulated	U-U16	0.6	-	-	-	No published sequence similarity
SEQ -ID-NO-36	Pulp Upregulated	U-U30	0.8	-	-	-	-
SEQ -ID-NO-37	Pulp Upregulated	U-U40	10	-	-	-	-
SEQ -ID-NO-38	Pulp Upregulated	U-U108	1.1	-	-	-	-

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Sequence Identity	Group	Clone no.	Size Kb	Published Sequence gene Identity	% Identity	Sequence Bp	Published Sequences
SEQ -ID-NO-39	Pulp Upregulated	U-U128	2.2	-	-	-	-
SEQ -ID-NO-40	Pulp Down regulated	U-D4	1.3	Granule Bond Starch Synthase	62.3	621	Cassava (<i>Manihot esculenta</i>), X74160
SEQ -ID-NO-41	Pulp Down regulated	U-D10	1.3	Starch Synthase	68.8	506	Pea (<i>Pisum sativum</i>), X88789
SEQ -ID-NO-42	Pulp Down regulated	U-D13	1.3	Starch Synthase	67.4	454	Pea (<i>Pisum sativum</i>), X88789
SEQ -ID-NO-43	Pulp Down regulated	U-D66	1.3	Granule Bond Starch Synthase	64.1	669	Cassava (<i>Manihot esculenta</i>), X74160
SEQ -ID-NO-44	Pulp Down regulated	U-D111	1.3	Starch Synthase	66.4	655	Cassava (<i>Manihot esculenta</i>), X74160
SEQ -ID-NO-45	Pulp Down regulated	U-D112	2.3	Granule Bond Starch Synthase	68.4	196	Potato (<i>Solanum tuberosum</i>), X58453